

DT12 Rec'd PCT/PTO 02 DEC 2004

SEQUENCE LISTING

<110> HARA, Takahito
KUSAKA, Masami
MIYAZAKI, Junichi

<120> Mutated Androgen Receptor, Cancer Cells Expressing Same,
Production Method Thereof and Use Thereof

<130> 3056US0P

<150> PCT/JP03/06942

<151> 2003-06-02

<150> JP 2002-162206

<151> 2002-06-03

<150> JP 2002-255612

<151> 2002-08-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2775)

<223>

<400> 1

atg gaa gtg cag tta ggg ctg gga agg gtc tac cct cgg ccg ccg tcc	48
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser	
1 5 10 15	
aag acc tac cga gga gct ttc cag aat ctg ttc cag agc gtg cgc gaa	96
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu	
20 25 30	
gtg atc cag aac ccg ggc ccc agg cac cca gag gcc gcg agc gca gca	144
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala	
35 40 45	
cct ccc ggc gcc agt ttg ctg ctg ctg cag cag cag cag cag cag cag	192
Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln	
50 55 60	
cag cag cag cag cag cag cag cag cag cag cag cag cag cag cag	240
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
65 70 75 80	
cag cag cag caa gag act agc ccc agg cag cag cag cag cag cag ggt	288
Gln Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly	
85 90 95	
gag gat ggt tct ccc caa gcc cat cgt aga ggc ccc aca ggc tac ctg	336
Glu Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu	
100 105 110	
gtc ctg gat gag gaa cag caa cct tca cag ccg cag tcg gcc ctg gag	384

Val	Leu	Asp	Glu	Glu	Gln	Gln	Pro	Ser	Gln	Pro	Gln	Ser	Ala	Leu	Glu		
		115					120					125					
tgc	cac	ccc	gag	aga	ggt	tgc	gtc	cca	gag	cct	gga	gcc	gcc	gtg	gcc	432	
Cys	His	Pro	Glu	Arg	Gly	Cys	Val	Pro	Glu	Pro	Gly	Ala	Ala	Val	Ala		
		130					135					140					
gcc	agc	aag	ggg	ctg	ccg	cag	cag	ctg	cca	gca	cct	ccg	gac	gag	gat	480	
Ala	Ser	Lys	Gly	Leu	Pro	Gln	Gln	Leu	Pro	Ala	Pro	Pro	Asp	Glu	Asp		
		145					150					155			160		
gac	tca	gct	gcc	cca	tcc	acg	ttg	tcc	ctg	ctg	ggc	ccc	act	ttc	ccc	528	
Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	Leu	Leu	Gly	Pro	Thr	Phe	Pro		
				165											175		
ggc	tta	agc	agc	tgc	tcc	gct	gac	ctt	aaa	gac	atc	ctg	agc	gag	gcc	576	
Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Leu	Lys	Asp	Ile	Leu	Ser	Glu	Ala		
				180											190		
agc	acc	atg	caa	ctc	ctt	cag	caa	cag	cag	cag	gaa	gca	gta	tcc	gaa	624	
Ser	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Glu	Ala	Val	Ser	Glu		
				195											205		
ggc	agc	agc	agc	ggg	aga	gcg	agg	gag	gcc	tcg	ggg	gct	ccc	act	tcc	672	
Gly	Ser	Ser	Ser	Gly	Arg	Ala	Arg	Glu	Ala	Ser	Gly	Ala	Pro	Thr	Ser		
				210											220		
tcc	aag	gac	aat	tac	tta	ggg	ggc	act	tcg	acc	att	tct	gac	aac	gcc	720	
Ser	Lys	Asp	Asn	Tyr	Leu	Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala		
															240		
aag	gag	ttg	tgt	aag	gca	gtg	tcg	gtg	tcc	atg	ggc	ctg	ggt	gtg	gag	768	
Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu		
															255		
gcg	ttg	gag	cat	ctg	agt	cca	ggg	gaa	cag	ctt	cgg	ggg	gat	tgc	atg	816	
Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met		
															270		
tac	gcc	cca	ctt	ttg	gga	gtt	cca	ccc	gct	gtg	cgt	ccc	act	cct	tgt	864	
Tyr	Ala	Pro	Leu	Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys		
															285		
gcc	cca	ttg	gcc	gaa	tgc	aaa	ggt	tct	ctg	cta	gac	gac	agc	gca	ggc	912	
Ala	Pro	Leu	Ala	Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly		
															300		
aag	agc	act	gaa	gat	act	gct	gag	tat	tcc	cct	ttc	aag	gga	ggt	tac	960	
Lys	Ser	Thr	Glu	Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr		
															320		
acc	aaa	ggg	cta	gaa	ggc	gag	agc	cta	ggc	tgc	tct	ggc	agc	gct	gca	1008	
Thr	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala		
															335		
gca	ggg	agc	tcc	ggg	aca	ctt	gaa	ctg	ccg	tct	acc	ctg	tct	ctc	tac	1056	
Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr		
															350		
aag	tcc	gga	gca	ctg	gac	gag	gca	gct	gcg	tac	cag	agt	cgc	gac	tac	1104	
Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr		
															365		
tac	aac	ttt	cca	ctg	gct	ctg	gcc	gga	ccg	ccg	ccc	cct	ccg	ccg	cct	1152	
Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro		
															380		
ccc	cat	ccc	cac	gct	cgc	atc	aag	ctg	gag	aac	ccg	ctg	gac	tac	ggc	1200	
Pro	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly		
															400		
agc	gcc	tgg	gcg	gct	gcg	gcg	gcg	cag	tgc	cgc	tat	ggg	gac	ctg	gcg	1248	
Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala		
															415		
agc	ctg	cat	ggc	gcg	ggt	gca	gcg	gga	ccc	ggt	tct	ggg	tca	ccc	tca	1296	

Ser	Leu	His	Gly	Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	
			420					425					430			
gcc	gcc	gct	tcc	tca	tcc	tgg	cac	act	ctc	ttc	aca	gcc	gaa	gaa	ggc	1344
Ala	Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	
			435					440					445			
cag	ttg	tat	gga	ccg	tgt	ggt	ggt	ggt	ggg	ggt	ggt	ggc	ggc	ggc	ggc	1392
Gln	Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
	450						455						460			
ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	gag	gcg	gga		1440
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	
	465					470				475					480	
gct	gta	gcc	ccc	tac	ggc	tac	act	cgg	ccc	cct	cag	ggg	ctg	gcg	ggc	1488
Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	
				485					490						495	
cag	gaa	agc	gac	ttc	acc	gca	cct	gat	gtg	tgg	tac	cct	ggc	ggc	atg	1536
Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	
			500					505					510			
gtg	agc	aga	gtg	ccc	tat	ccc	agt	ccc	act	tgt	gtc	aaa	agc	gaa	atg	1584
Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	
			515				520						525			
ggc	ccc	tgg	atg	gat	agc	tac	tcc	gga	cct	tac	ggg	gac	atg	cgt	ttg	1632
Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	
	530					535					540					
gag	act	gcc	agg	gac	cat	gtt	ttg	ccc	att	gac	tat	tac	ttt	cca	ccc	1680
Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	
	545				550					555					560	
cag	aag	acc	tgc	ctg	atc	tgt	gga	gat	gaa	gct	tct	ggg	tgt	cac	tat	1728
Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	
			565						570					575		
gga	gct	ctc	aca	tgt	gga	agc	tgc	aag	gtc	ttc	ttc	aaa	aga	gcc	gct	1776
Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	
			580					585					590			
gaa	ggg	aaa	cag	aag	tac	ctg	tgc	gcc	agc	aga	aat	gat	tgc	act	att	1824
Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	
		595				600						605				
gat	aaa	ttc	cga	agg	aaa	aat	tgt	cca	tct	tgt	cgt	ctt	cgg	aaa	tgt	1872
Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	
	610				615						620					
tat	gaa	gca	ggg	atg	act	ctg	gga	gcc	cgg	aag	ctg	aag	aaa	ctt	ggt	1920
Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	
	625				630				635					640		
aat	ctg	aaa	cta	cag	gag	gaa	gga	gag	gct	tcc	agc	acc	acc	agc	ccc	1968
Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	
			645						650					655		
act	gag	gag	aca	acc	cag	aag	ctg	aca	gtg	tca	cac	att	gaa	ggc	tat	2016
Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	
			660					665					670			
gaa	tgt	cag	ccc	atc	ttt	ctg	aat	gtc	ctg	gaa	gcc	att	gag	cca	ggt	2064
Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	
		675					680					685				
gta	gtg	tgt	gct	gga	cac	gac	aac	aac	cag	ccc	gac	tcc	ttt	gca	gcc	2112
Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	
		690				695					700					
ttg	ctc	tct	agc	ctc	aat	gaa	ctg	gga	gag	aga	cag	ctt	gta	cac	gtg	2160
Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	
	705				710					715					720	
gtc	aag	tgg	gcc	aag	gcc	ttg	cct	ggc	ttc	cgc	aac	tta	cac	gtg	gac	2208

Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	
			725						730					735		
gac	cag	atg	gct	gtc	att	cag	tac	tcc	tgg	atg	ggg	ctc	atg	gtg	ttt	2256
Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	
			740						745					750		
gcc	atg	ggc	tgg	cga	tcc	ttc	acc	aat	gtc	aac	tcc	agg	atg	ctc	tac	2304
Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	
			755					760				765				
ttc	gcc	cct	gat	ctg	gtt	ttc	aat	gag	tac	cgc	atg	cac	aag	tcc	cgg	2352
Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg	
			770				775					780				
atg	tac	agc	cag	tgt	gtc	cga	atg	agg	cac	ctc	tct	caa	gag	ttt	gga	2400
Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly	
			785			790				795					800	
tgg	ctc	caa	atc	acc	ccc	cag	gaa	ttc	ctg	tgc	atg	aaa	gca	ctg	cta	2448
Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu	
				805					810					815		
ctc	ttc	agc	att	att	cca	gtg	gat	ggg	ctg	aaa	aat	caa	aaa	ttc	ttt	2496
Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe	
			820					825					830			
gat	gaa	ctt	cga	atg	aac	tac	atc	aag	gaa	ctc	gat	cgt	atc	att	gca	2544
Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala	
			835				840					845				
tgc	aaa	aga	aaa	aat	ccc	aca	tcc	tgc	tca	aga	cgc	ttc	tac	cag	ctc	2592
Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu	
			850				855					860				
acc	aag	ctc	ctg	gac	tcc	gtg	cag	cct	att	gcg	aga	gag	ctg	cat	cag	2640
Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln	
					870					875					880	
ttc	act	ttt	gac	ctg	cta	atc	aag	tca	cac	atg	gtg	agc	gtg	gac	ttt	2688
Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe	
				885					890					895		
ccg	gaa	atg	atg	gca	gag	atc	atc	tct	gtg	caa	gtg	ccc	aag	atc	ctt	2736
Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu	
				900					905					910		
tct	ggg	aaa	gtc	aag	ccc	atc	tat	ttc	cac	acc	cag	tga				2775
Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	His	Thr	Gln					
			915					920								

<210> 2
 <211> 924
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1 5 10 15
 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30
 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly

				85					90					95			
Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Arg	Arg	Gly	Pro	Thr	Gly	Tyr	Leu		
			100					105					110				
Val	Leu	Asp	Glu	Glu	Gln	Gln	Pro	Ser	Gln	Pro	Gln	Ser	Ala	Leu	Glu		
		115					120					125					
Cys	His	Pro	Glu	Arg	Gly	Cys	Val	Pro	Glu	Pro	Gly	Ala	Ala	Val	Ala		
	130					135					140						
Ala	Ser	Lys	Gly	Leu	Pro	Gln	Gln	Leu	Pro	Ala	Pro	Pro	Asp	Glu	Asp		
145					150					155					160		
Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	Leu	Leu	Gly	Pro	Thr	Phe	Pro		
				165					170					175			
Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Leu	Lys	Asp	Ile	Leu	Ser	Glu	Ala		
			180					185					190				
Ser	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Glu	Ala	Val	Ser	Glu		
		195					200					205					
Gly	Ser	Ser	Ser	Gly	Arg	Ala	Arg	Glu	Ala	Ser	Gly	Ala	Pro	Thr	Ser		
	210					215					220						
Ser	Lys	Asp	Asn	Tyr	Leu	Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala		
225					230					235					240		
Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu		
			245						250					255			
Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met		
			260					265					270				
Tyr	Ala	Pro	Leu	Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys		
	275						280					285					
Ala	Pro	Leu	Ala	Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly		
	290					295					300						
Lys	Ser	Thr	Glu	Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr		
305					310					315					320		
Thr	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala		
			325						330					335			
Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr		
			340					345					350				
Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr		
	355						360					365					
Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro		
	370					375					380						
Pro	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly		
385					390					395					400		
Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala		
			405						410					415			
Ser	Leu	His	Gly	Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser		
			420					425					430				
Ala	Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly		
	435						440					445					
Gln	Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly		
	450					455					460						
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	
465						470				475					480		
Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly		
				485				490						495			
Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met		
			500					505				510					
Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met		
	515						520					525					
Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu		
	530					535					540						

Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro
545					550					555					560
Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr
				565					570						575
Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala
			580					585					590		
Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile
		595					600					605			
Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys
	610					615					620				
Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly
625					630					635					640
Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro
				645					650					655	
Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr
			660					665					670		
Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly
		675					680					685			
Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala
	690					695					700				
Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val
705					710					715					720
Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp
				725					730					735	
Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe
			740					745					750		
Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr
		755					760					765			
Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg
	770					775					780				
Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly
785					790					795					800
Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu
				805					810					815	
Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe
			820					825					830		
Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala
		835					840					845			
Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu
	850					855					860				
Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln
865					870					875					880
Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe
				885					890					895	
Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu
			900					905					910		
Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	His	Thr	Gln				
		915					920								

<210> 3
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<223> ARE sequence in human PSA promoter.

<400> 3

agaacagcaa gtgct

15

<210> 4

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> ARR sequence in human PSA promoter.

<400> 4

gtggtgcagg gatcagggag tctcacaatc tcctg

35

<210> 5

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as primer for amplifying human
PSA promoter.

<400> 5

ggagctcgaa ttccacattg tttgctgcac gttgg

35

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as primer for amplifying human
PSA promoter.

<400> 6

caagctttgg ggctggggag cctccccag gagc

34